

Figure 1

SEQ ID 8	CTAAGCC CTCAGAACCGTCTCGGA (→)
AF196835	CAACCCAGGAGGACTGGGTGAACAAAGCCGCGAAGTGA TCCATGTAAGCC CTCAGAACCGTCTCGGAAGGAGGACCCACATGTTGTAACTTCAAAG
AF260968T.....
AF260969
AF481864
M12294C.....T.....G.C.T.G.C.....
AF206518
AF317203
AF202541
AF404757T.....
AF404753
AF404754
AF404755
AF404756
AF017254T.....
L48977C.....T.....G.....C.....G.C.T.G.C.....
AF196536
AF196537T.....G.C.....T.....G.C.....
AF196538T.....G.C.....T.....GT.C.....
AF196540T.....G.C.....T.....GT.C.....
AF196541
AF196542
AF196543T.C.....G.....C.....A.....G.....T.G.C.....G.....
AF297840T.....C.....A.....G.....G.....G.....
AF458343C.....G.....
AF458344T.....
AF458347T.....
AF458348
AF458350
AF458352T.G.C.....C.....T.....GT.Y.....
AF458353T.G.C.....T.....GT.C.....
AF458355T.....
AF458358T.C.....G.....C.....A.....G.....T.G.C.....G.....
AF458360
AF458361
AF208017C.....T.....G.....C.....G.C.T.G.C.....
AF196539C.....T.....G.....C.....G.C.T.G.C.....
AF196535C.....T.....G.....C.....G.C.T.G.C.....G.....
AF458359C.....T.....G.....C.....G.C.T.G.C.....
AF458357C.....T.....G.....C.....G.C.T.G.C.....
AF458354C.....T.....G.....C.....G.C.T.G.C.....

[illegible]

AF458351T.....G.A.....G.....G.....
AF458356T.....C.....A.....G.....G.....
L24512T.....A.....G.....G.....
JEV
AB051292	..GTT.....
AF014160	..GT.....
AF014161	..GT.....
AF045551	..GTT.....
AF069076	..GT.....
AF075723	..GT.....
AF080251	..GT.....
AF098735	..GT.....
AF098736	..GT.....
AF098737	..GT.....
AF217620	..GTT.....
AF221499	..GT.....
AF221500	..GT.....
AF254452	..GT.....
AF254453	..GT.....
AF315119	..GT.....
AF416457	..GT.....
AF486638	..GT.....
U14163	..GT.....
U15763	..GT.....
L48961	..GT.....
U47032	..GT.....
M18370	..GT.....
M55506	..GT.....
D90195	..GT.....
D90194	..GT.....
AF311748	..GT.....
AF092550	..GTT.....
AF092552	..GTT.....
AF092553	..GTT.....
AF139531	..GTT.....
AF148900	..GTT.....
AF148901	..GTT.....
AF148902	..GTT.....
AF218068	..GTT.....
AF289816	..GT.....
AF318291	..GT.....
L48967	..GTT.....
L48968	..GTT.....

AY184212	..GT.....	C.....	T.T.AC.CG.GAGTGA.A.....	A.....	T.....	TG.TCAC.G.TG..GG...
AY251616	..GT.....	T.....	T.T.AC.CG.AGGTGG.A.....	T.....	T.....	TG.TCAC.G.G.G.....
AY278556	..GTT.....	T.....	T.T.AC.CG.AGGTGG.A.....	C.....	T.....	TG.TCAC.G.G.G.....
AY316157	..GTT.....	T.....	T.T.AC.CG.AGGTGG.A.....	A.....	T.....	TG.TCAC.G.G.G.....
L54067	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54068	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54069	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54070	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54071	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54072	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54122	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
L54123	..GTT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
AF306514	..GTT.....	T.....	T.T.AC.CG.AGGTGG.A.....	CTCCT.....	T.....	TG.TCAC.G.G.G.....
AF306515	..GT.....	C.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
AF306516	..TT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
AF306517	..GT.....	T.....	T.T.AC.CA.AGGTGA.A.....	T.....	T.....	TG.TCAC.G.G.G.....
SLEV						
BFS1750-C	TGG.....	T.T.....	AATCT.GCCGAGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
1750-Std	TGG.....	T.T.....	AATCT.GCCGAGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
TD6-4G-C	TGG.....	T.T.....	AATCT.GCCGAGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
TD6-4G-20	TGG.....	T.T.....	AATCT.GCCGAGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
CoaV750	TGG.....	T.T.....	AATCT.GCTGAGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
L695121.05	TGG.....	T.T.....	AATCC.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
TNM771K-C	TGG.....	T.T.....	AATCT.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
MSI-7-C	TGG.....	C.T.....	AATCC.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
Kern217	TGG.....	C.....	AATCC.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
CoaV608	TGG.....	C.....	AATCC.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
TBH-28	TGG.....	T.....	AATCC.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
VR1265	TGG.....	T.....	AATCT.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
CoaV353	TGG.....	T.....	AATCT.GCTGGGT.GCA.....	C.....	TT.A.....	GTCC.TAGCACGTAG.CTGGAGAGG.C
MVEV						
VR77						
AF161266	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
M35172	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
L48972	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
L48973	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
L48974	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
L48975	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
L48976	T.C.....	T.ATTCTCC.CGGTTG.A.....	T.C.....	AG.AGT.....	TGCCAACAAATGGAGATG.A
Koutango virus						
L48980	C.....	T.T....G.A....C....T.....			G....T.TTC.....

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[illegible]

AF416457	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
AF486638	CCC.C	AGG.T	A.	CAT	TTG.T	A.T.G
U14163	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
U15763	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
L48961	CTC.C	AGG.T	A.	CAT	TTG.T	A..G
U47032	CCC.C	AGG.T.G	A.	CAT	TTG.T	A..G
M18370	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
M55506	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
L78128	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
D90195	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
D90194	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
AF311748	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
AY184212	CCCT.C	AAG.T	A.	CAT	TTG.T	A..G
AY316157	CCC.C	AGG.T	A.	CAA	TTG.T	A..G
AF306514	CCC.C	AGG.T.T	A.	CAA	TTG.T	A..G
AF306515	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
AF306516	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
AF306517	CCC.C	AGG.T	A.	CAT	TTG.T	A..G
D00037	CCT.T.T	T.T.AGGT.TT	T.T	CT	TTG.T	A..G
M14933	CCT.T.T	T.T.AGGT.TT	T.T	CT	TTG.T	A..G
SLEV						
BFS1750-C	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
1750-Std	CCG.C	AGAC.G	A.	C.GA		
TD6-4G-C	CCG.C	AGAT.G	A.	T..G.TT..G.	A.	A.
TD6-4G-20	CCG.C	AGAT.G	A.	T..G.TT..G.	A.	A.
CoaV750	CCG.C	AGAT.G	A.	C.G		
L695121.05	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
TNM771K-C	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
MSI-7-C	CCG.CA	AGAC.G	A.	T..G.TT..G.	A.	A.
Kern217	CCG.CA	AGAC.G	A.	T..G.TT..G.	A.	A.
CoaV608	CCG.CA	AGAC.G	A.	T..G.TT..G.	A.	A.
TBH-28	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
VR1265	CCG.C	AGAC.G	A.	T..G.TC..G.	A.	A.
CoaV353	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
MVEV						
VR77	.CG.C	A.G.G.T.C	A.	ACT.T	.C	AA.
AF161266	.CG.C	A.G.G.T.C	A.	ACT.T	.C	AA.
M35172	.CG.C	A.G.G.T.C	A.	ACT.T	.C	AA.

[illegible]

AY268133G.....
 AY490240
 Kunjin virus
 AY274504 ...A.T.....T.C.G....
G.....
 AY274505 ...A.T.....T.C.G....
G.....
 L24512 ...A.T.....T.C.G....
G.....
 Japanese encephalitis virus
 AB051292 .TA..T.T.....T... AAA C.CA TT .TG.....AG.CCC..
 C.....G.AGG...T.....A.....CATTGC.TCA.
 AF014160 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF014161 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF045551 TTA..T.T.....T... AAA C.AA TT .TG.....AG.CCC..
 C.....AGG...T.T... A.....CAATTGC.T..
 AF069076 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF075723 .GA..T.T.....T... AAA T.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF080251 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF098735 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CTC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF098736 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF098737 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF217620 .GA..T.T.....T... AAA C.CA AT .TG.....AG..TC..
 C.....AGG.A.T.....A.....CATTGC.TCA.
 AF221499 .GA..T.T.....T... AAA C.TA A. .TG.....AG.CTC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF221500 .GA..T.T.....T... AAA C.TA A. .TG.....AG.CTC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF254452 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF254453 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF315119 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF416457 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 AF486638 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.
 U14163 .GA..T.T.....T... AAA C.CA A. .TG.....AG.CCC..
 C.....AGG...T.....A.....CATTGC.TCA.

U15763	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
L48961	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CTC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
U47032	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T..G.....	A.....	CATTGC.TCA.				
M18370	.GA..T.T.....T..	AAA	C..CA	AT		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
M55506	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
L78128	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
D90195	.GA..T.T.....T..	AAA	C..CA	AT		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
D90194	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AF311748	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AY184212	.GA..AT.T.....T..	AAA	C..CA	A.		.TG.....AG.CCCT.
C.....	AAG..T.....	A.....	CAT.TGC.TCA.				
AY316157	.TA..T.T.....T..	AAA	C..CA	T.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CAATTGC.T..				
AF306514	.TTA..T.T.....T..	AAA	C..AA	TT		.TG.....AG.CCC..
C.....	AGG..T.T.....	A.....	CAATTGC.T..				
AF306515	.GA..T.T.....T..	AAA	C..AA	AA		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AF306516	.GA..T.T.....T..	AAA	C..AA	AA		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AF306517	.GA..T.T.....T..	AAA	C..AA	AA		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
St. Louis encephalitis virus							
BFS1750	..T...T.....T..	CA	.CTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				
1750-Std	..T...T.....T..	CA	.CTTG	..		.A.....AA.CCG..C
TD6-4G	..T...T.....T..	CA	.CTCG	..		.A.....AA.CCG..C
.....	AGAT..G.....	A.....	T...GTT..CGC				
CoaV750	..T...T.....T..	CA	.CTTG	..		.A...A.AA.CCG..C
L695121.05	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				
TNN771K	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				
MSI-7	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
A.....	AGAC..G.....	A.....	T...GTT..CGC				
Kern217	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
A.....	AGAC..G.....	A.....	T...GTT..CGC				
CoaV608	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
A.....	AGAC..G.....	A.....	T...GTT..CGC				
TBH-28	..T...T.....T..	.A	.TTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				

VR1265 ..T...T.....T.....T..A..CTTG .. . A.....AA.CCG..C
AGAC..G.....A.....T....GTC..CGC
 CoaV353 ..T...T.....T.....T..CA..CTTG .. . A.....AA.CCG..C
AGAC..G.....A.....T....GTT..CGC
 Murray Valley encephalitis virus
 VR77 ..CC.....T.....T....AAGA G T.....AG..CG.CA.G.G..T..C.....A.....ACT.T
GC
 AF161266 ..CC.....T.....T....AAGA G T.....AG..CG.CA.G.G..T..C.....A.....ACT.T
GC
 M35172 ..CC.....T.....T....AAGA G T.....AG..CG.CA.G.G..T..C.....A.....ACT.T
GC
 Dengue virus type 1
 U88537 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 U88536 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 U88535 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 M87512 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....TCCTG.TG.T.....A.....CG..ATA.C..T. GCGG.....A.ACC.GG
 AY206457 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C... GCGG.....A
 AY145123 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
A.....CC..ACA.C... GCGG.....A.ACC.GG
 AY145122 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CTC.T.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AY145121 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CTC.T.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AF514889 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AF514885 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ATA.C... GCGG.....A.ACC.GG
 AF514883 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ATA.C... GCGG.....A.ACC.GG
 AF514878 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AF514876 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ATA.C... GCGG.....A.ACC.GG
 AF513110 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AF350498 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ATA.C..T. GCGG.....A.ACC.GG
 AF311958 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..TCA.C... GCGG.....A.ACC.GG
 AF311957 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AF311956 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C... GCGG.....A.ACC.GG
 AF310148 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG G.....CCTG.TG.T.....

AF310147	AT...GT.GCA.....T.....	T.CCAAAAC	AC..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..ATA.C.T.		
AF310146	AT...GT.GCA.....T.....	T.CCTAGAC	AT..CGCAGCA	GCGG.....A.ACC.TG
G.....	CC.TG.TG.T.....A.....	CC..ACA.C....		
AF309641	AT...GT.GCA.....T.....	T.CCGAAAC	AT..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..ATA.C.T.		
AF298808	AT...GT.GCA.....T.....	T.CCAAAAC	AC..CGCAGCA	GCGG.....A.ACT.GG
G..T.....	CCCTG.TG.T.....A.....	CC..ATA.C.T.		
AF298807	AT...GT.GCA.....T.....	T.CCAAAAC	AT..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..ACA.C....		
AF226687	AT...GT.GCA.....T.....	T.CCAAGAC	AT..CGCAGCA	GCGG.....A.ACC.GG
G.....	CC.TG.TG.T.....A.....	CC..ACA.C....		
AF226686	AT...GT.GCA.....T.....	T.CCAAGAC	AT..CGCAGCA	GCGG.....A.ACC.GG
G.....	CC.TG.TG.T.....A.....	CC..ACA.C....		
AF226685	AT...GT.GCA.....T.....	T.CCTAGAC	AT..CGCAGCA	GCGG.....A.ACC.TG
G.....	CC.TG.TG.T.....A.....	CC..ACA.C....		
AF180818	AT...GT.GCA.....T.....	T.CCAAGAC	AC..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..GTA.C.T.		
AF180817	AT...GT.GCA.....T.....	T.CCAAGAC	AC..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..GTA.C.T.		
AB074761	AT...GTTGCA.....T.....	T.CCAAGAC	AC..CGCAGCA	GCGG.....A.ACC.GG
GA.....	CCCTG.TG.T.....A.....	CC..ATA.T.T.		
AB074760	AT...GT.GCA.....T.....	T.CCAAAAC	AC..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..ATA.C.T.		
VR344-3	AT...GT.GCA.....AT.....	T.CCAAGAC	AC..CGCAGCA	GCGG.....A.ACC.GG
G.....	CCCTG.TG.T.....A.....	CC..ATA.C.T.		
Dengue virus type 2				
AF022434	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C.GA.				
AF022435	AT..CGT.GT.....C.....	T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF022436	AT..CGT.GT.....C.....	T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF022437	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF022438	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF022439	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF022440	AT..CGT.GT.....C.....	T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF022441	AT..CGT.GT.....C.....	T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....	CCCCGA
A.C..A.				
AF038402	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....	CCCCAA
A.C..A.				
AF038403	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....	CCCCAA
A.C..A.				
AF100145	AT..CGT.GT.....C.....	T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....	CCCCAA
A.T..A.				

AF100146 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 AGC..A.
 AF100147 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100148 AT..TGT.GT.....C.....T.CCTT C AG.TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF100149 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA T.....CCTCACT.....A.....CCCAA
 A.C..A.
 AF100150 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF100151 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 G.C..A.
 AF100458 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA
 T.....TCTCACT.....A.....CCCAA.A.C..A.
 AF100459 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100460 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100461 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100462 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100463 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100464 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGCA.GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100465 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 G.C..A.
 AF100466 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.T..A.
 AF100467 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA
 T.....TCTCACT.....A.....CCCAA.A.C..A.
 AF100468 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA
 T.....TCTCACT.....A.....CCCAA.A.C..A.
 AF100469 AT..CGT.GT.....C.....T.CCTT C AG.TCGAGCAACAATGGG.....TGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF119661 AT..CGT.GG.....C.....T.CCTT AC A..TCGAGCAACAACGGG.....AGG...GA T.....TCTCACT.....ATT.....CCCAA
 A.C..A.
 AF169687 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF169678 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF169688 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF169679 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AAG...GA T.....TCTCACT.....A.....CCCGA
 A.C..A.
 AF169680 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CTT.....A.....CCCGA
 A.C..A.

AF169681 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169682 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169683 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169684 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169685 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169686 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF204177 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.
AF204178 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.
AF208496 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.
AF276619 AT..CGT.GT.....C.....T.CCTT GC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309950 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309951 AT..CGT.GT.....C.....T.CCTT AC AG.TCGCAGCAACAACGGG.....AGG...GA TA.....TCTCACC.....A.....CCCAA
A.C..A.
AF305592 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309953 GT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAAAAATGGG.....AGG..TG.
T.....CCCACT.....A.....CCAG.....A.
AF309954 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAAAAATGGG.....AGG..TG.
T.....CCCACT.....A.....CCAG.....A.
AF309955 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309956 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309957 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309958 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309959 AT..TGT.GT.....C.....T.CCTT AA A..TCGCAGCAAAAATGGG.....AGG..TGG T.....CCCACT.....A.....CCCAG
AC...A.
AF309960 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309961 AT..TGT.GT.....C.....T.CCTT AA GG.TCGCAGCAA AATGGG.....AGG..TGG T.....CCCACT.....A.....CCCA.
A..T.AT
AF309962 AT..CGT.GT.....C.....T.CCTT GC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309963 AT..CGT.GT.....C.....T.CCTT AC A..GTGCGAGCAGCAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.

AF309964	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.		
AF309965	AT..CGT.GT.....C.....T.CCTT .C	AG.TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
AF359579	AT..CGT.GT.....C.....T.CCTT GC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.		
AF489932	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
AJ487271	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
AY037116	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.A.....A.....CCCGA
A.T..A.		
M19197	AT..CGT.GT.....C.....T.CCTT AC	AG.TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
M20558	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
M29095	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
M84727	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
M84728	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U61245	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C.GA.		
U61246	AT..CGT.GT.....C.....T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U61247	AT..CGT.GT.....C.....T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U61248	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U87411	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U87412	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
VR345-2	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TC.C.CT.....A.....CCCGA
A.C..A.		
<u>Dengue virus type 3</u>		
AF310149	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		
M93130	AC..TGT.GCA.....T.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....TA.....CC..A
A.C... .		
AF317645	AC..TGT.GCA.....T.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....TA.....CC..A
A.C... .		
AY099336	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		
AY099337	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		
AY099343	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		

AY099344	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GC GG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T...							
AY099345	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GC GG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T...							
AY099346	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GC GG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T...							
AY099347	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GC GG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T...							
VR1256-3	AC..TGT.GCA.....T.....	T.CCATGAC	AC..CGCAGCA	GC GG.....GAG.ACTGAGG.....	CC..CTTGCA.....	TA.....	CC..A
A.C...							
VR1256-5	AC..TGT.GCA.....T.....	T.CCATGAC	AC..CGCAGCA	GC GG.....GAG.ACTGAGG.....	CC..CTTGCA.....	TA.....	CC..A
A.C...							
Dengue virus type 4							
M14931	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AF289029	GT..CAT.TT.....C.....	T.CCATCACCACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AF310150	GT..CAT.TT.....T.....	T.CCATTA.CAACA...	CGCAGCAC	AA.GGG.....GAAG.C.GGAT.....	CTC.T.AT.....		
AF310152	GT..CAT.TT.....T.....	T.CCATTA.CAACA...	CGCAGCAC	AA.GGG.....GAAG.C.GGAT.....	CTC.T.AT.....		
AF310153	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AF326573	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AF326825	GT..CAT.TT.....C.....	T.CCATCACTGATA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AF326826	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....A.....		A.....	CCCAACA
C...							
AF326827	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....A.....		A.....	CCCAACA
C...							
AF375822	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152039	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152043	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152047	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152051	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152055	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152059	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152063	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152067	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							
AY152071	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C...							

[illegible]

[illegible]

[illegible]

AY152171	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....	GAAGCC.GGAG.....	CTC.T..T.....	A.....	CCCAACA
C...:								
VR217-1	GT..CAT.TT.....C.....	T.CCATCACTAACA...	CGCAGCA	AAAGGGG.....	GAAGCC.GGAG.....	CTC.T..T.....	A.....	CCCAACA
C...:								

*Two potential binding sites for SEQ ID NOS.: 28 & 70 can be found in this region. These are denoted by single underline for SEQ ID NO.: 28, and shading for SEQ ID NO.: 70.

KY1129 5'-GTAAGCC CTCAGAACCGTCTCGGAA-3'

WNV

AF317203
AF196835
AF260967
AF260968
AF260969
AF481864
M12294
AF206518
AF317203
AF202541
AF404757
AF404753
AF404754
AF404755
AF404756
AF017254
L48977
AF196536
AF196537
AF196538
AF196540
AF196541
AF196542
AF196543
AF458343C.....
AF458344
AF458347
AF458348
AF458350
AF458352C.....
AF458353
AF458355
AF458358
AF458360
AF458361
AF208017
AF196539
AF196535
AF458359
AF458357
AF458354
AF458349
AF458345
AF458346T.....T.....
AF533540

JEV

AB051292	.A.....
AF014160	.A.....
AF014161	.A.....
AF045551	.A.....
AF069076	.A.....
AF075723	.A.....
AF080251	.A.....G.....
AF098735	.A.....
AF098736	.A.....
AF098737	.A.....
AF217620	.A.....
AF221499	.A.....
AF221500	.A.....
AF254452	.A.....
AF254453	.A.....
AF315119	.A.....T.....
AF416457	.A.....
AF486638	.A.....
U14163	.A.....
U15763	.A.....

Fig. 4A

KY1129 5'-GTAAGCC CTCAGAACCGTCTCGGAA-3'

JEV cont.

L48961	.A.....
U47032	.A.....
M18370	.A.....
M55506	.A.....
L78128	.A.....
D90195	.A.....
D90194	.A.....
AF311748	.A.....
AF092550	.A.....
AF092552	.A.....
AF092553	.A.....
AF139531	.A.....
AF148900	.A.....
AF148902	.A.....
AF218068	.A.....
AF289816	.A.....
AF318291	.A.....
L48967	.A.....
L48968	.A..C.....
L54067	.A.....
L54068	.A.....
L54069	.A.....
L54070	.A.....
L54071	.A.....
L54072	.A.....
L54122	.A.....
L54123	.A.....
AF306514	.A.....
AF306515	.A.....T.....
AF306516	.A.....T.....
AF306517	.A.....A.....T.....

MVEV

AF161266	.A.....T.C.....
M35172	.A.....T.C.....
L48972	.A.....T.C.....
L48973	.A.....T.C.....
L48974	.A.....T.C.....C.....
L48975	.A.....T.C.....
L48976	.A.....T.C.....T.....

KUNJIN

AF458351G.
AF458356
AF297840C.....
AF297841
AF297842
AF297843
AF297844
AF297845
AF297846C.....
AF297847C.....
AF297848
AF297849
AF297850C.....
AF297851C.....GT
AF297852C.....
AF297853C.....
AF297854
AF297855
AF297856
AF297857G.....
AF297858
AF297859
L48978
L49311
D00246
L48979
L24512

KOUTANGO

L48980
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Fig. 4B

KY1130 5'-TCCTAGTCTA TCCCAGGTGTCAA-3'

WNV

AF196835
AF260967
AF260968
AF260969
AF481864
M12294	C.....
AF206518
AF317203
AF202541
AF404757
AF404753
AF404754
AF404755
AF404756
AF017254A.....
L24512

JEV

AB051292	...C.....T.....
AF014160	...C.....T.....
AF014161	...C.....T.....
AF045551	...C.C...T.....
AF069076	...C.....T.....
AF075723	...C.....T.....
AF080251	...C.....T.....
AF098735	...C.....T.....
AF098736	...C.....T.....
AF098737	...G.....TCT.....
AF217620	...C.....T.....
AF221499	...C.....T.....
AF221500	...C.....T.....
AF254452	...C.....T.....
AF254453	...C.....T.....
AF315119	...C.....T.....
AF416457	...C.....T.....
AF486638	...C...A..T.....
U14163	...C.....T.....
U15763	...C.....T.....
L48961	...C.....T.....
U47032T.....
M18370	...C.....T.....
M55506	...C.....T.....
L78128	...C.....T.....
D90195	...C.....T.....
D90194	...C.....T.....
AF311748	...C.....T.....
AF306514	...C.C...T.....
AF306515	...C.....T.....
AF306516	...C.....T.....
AF306517	...C.C...T.....
D00037	...C.....T.....
M14933	...C.....T.....

MVEV

AF161266TT.....
M35172TT.....

Fig. 4C

KY1131 5' -GGACTAGAGGTTAGAGGAGACCCCGCGG-3'

WNV

AF196835
AF260967
AF260968
AF260969
AF481864
M12294T
AF206518
AF317203
AF202541
AF404757
AF404753
AF404754
AF404755
AF404756
AF017254
AF208017T.....A..T
L24512T

JEV

AB051292T..
AF014160T..
AF014161T..
AF045551T..
AF069076T..
AF075723T..
AF080251T..
AF098735T..
AF098736T..
AF098737T..
AF217620T..
AF221499T..
AF221500T..
AF254452T..
AF254453T..
AF315119T..
AF416457T..
AF486638T..
U14163T..
U15763T..
L48961T..
L24512
U47032T..
M18370T..
M55506T..
L78128T..
D90195T..
D90194T..
AF311748T..
AF306514T..
AF306515T..
AF306516T..
AF306517T..

MVEV

AF161266A.TC
M35172A.TC

Fig. 4D

KY1131 5' -GGACTAGAGGTTAGAGGAGACCCCGCGG-3'

DENGUE

AF226685C..C
AF311956C..C
AF311957C..C
AF311958C..C
AY145121C..C
AY145122C..C
AF514878C..C
AF514885C..C
AF514889C..C
AF489932C.CA
AF226687C..C
AX224213C.C.
AX224215C.C.
AX224217C.C.
AX224219C.C.
AX224225C.C.
AX224227C..C
AX224233C..C
AB074760C..C
AB074761C..C
A75711CG.C
AX224221C.C.
AX224223C.C.
U87412C.C.
U61246C.C.
U61247C.C.
AF100465C.CA
AF100466C.CA
AX224209C..C
AF180818C..C
AF326573C.CA
AF350498C..C
AF359579C.C.
AY037116C.C.
AF309950C.C.
AF309953C.CA
AF309954C.CA
AF309959C.CA
AF309962C.C.
AF309963C.C.
AF309964C.C.
AF309965C.CA
AF289029C.CA
AF208496C.CA
AF310146C..C
AF310149C..C
AF310153C.CA
AF226686C..C
AF276619C.C.
AF169678C.C.
AF169679C.C.
AF169680C.C.
AF169681C.C.
AF169682C.C.
AF169683C.C.
AF169684C.C.
AF169685C.C.
AF169686C.C.
AF169687C.C.
AF169688C.C.
AF100145C.CA
AF100467T.CC
AF100468T.CC
AF100149T.CC
M20558C.CA
M29095C.CA
M19197C.CA
M14931C.CA
U87411C.C.
U88536C..C

Fig. 5A

KY1131 5'-GGACTAGAGGTTAGAGGAGACCCGCGG-3'

DENGUE, cont.

U88537C..C
AF038403C.CA
AF326826C.CA
AF326827C.CA

MONTANA MYOTIS LEUKOENCEPHALITIS VIRUS

NC_004119TTCC
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MODOC VIRUS

NC_003635CG.C
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YELLOW FEVER VIRUS

X03700	..T.....TC.A.
U52393	..T.....TC.A.
U52407	..T.....TC.A.
AF052448	..T.....TC.A.

Fig. 5B

FIGURE 6

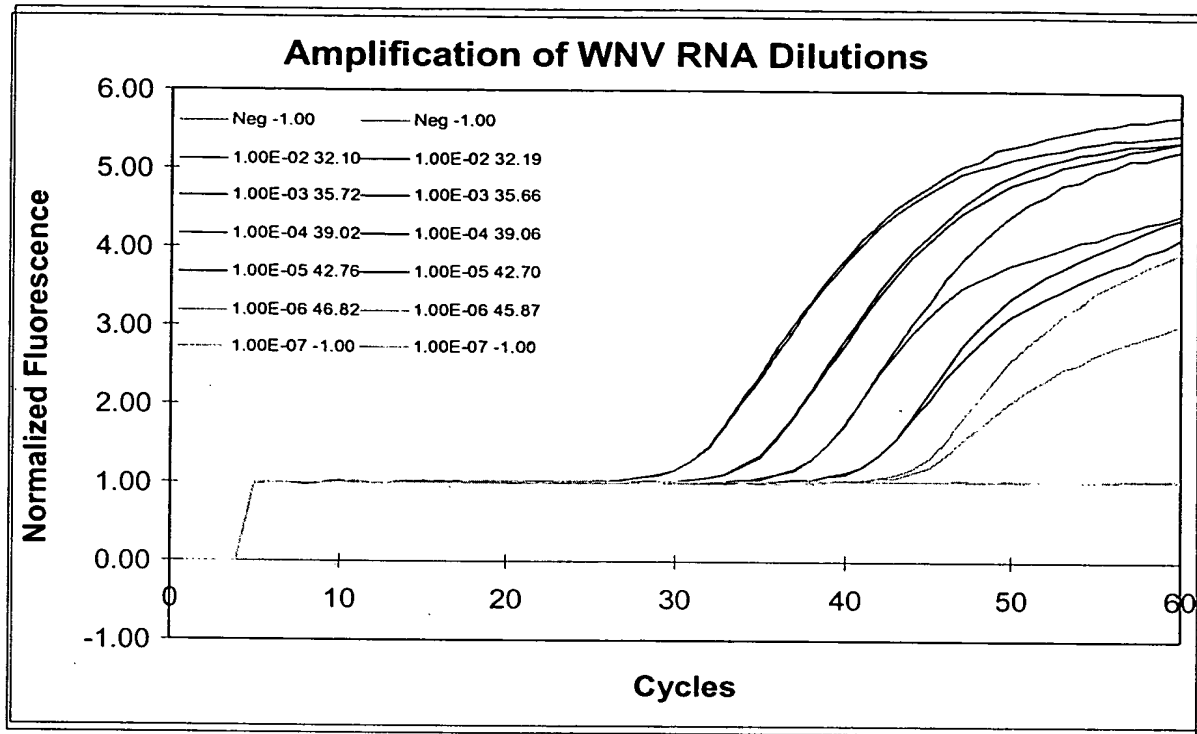


Figure 7

BFS1750	TTGCCACCGGATGTCAGGTAAACGGTGCTGTCTGTAACTGGCCCCCAGGTGACTGGGTTATCAAAGCCAATCTGGCCGAGTGCAAAAGCCC	90
1750-Std	
TD6-4GC.....	
CoaV750C.....C.....T.....	
L695121.05C.....C.....T.G.....	
TNM771KC.....C.....T.G.....	
MSI-7C.....C.....T.G.....	
Kern217C.....C.....T.G.....	
CoaV608C.....C.....T.G.....	
TBH-28C.....C.....T.G.....	
VR1265A.....T.G.....	
CoaV353A.T.....	
BFS1750	CTCATTCGGACTCGGGAGGTCCTTAGCACGTAGCTGGAGAGGACGCAAAAGTCAGACCAGAAATGCCACCTGAAAGCATGCTAAAGGT	180
1750-StdG.....	
TD6-4GG.....	
CoaV750	...G...T.....G.....	
L695121.05G...T.....C.....	
TNM771KG.....C.....	
MSI-7G.....C.....	
Kern217G.....C.....	
CoaV608G.....C.....	
TBH-28G.....C.....C.....	
VR1265G.....C.....C.....	
CoaV353G.....	
BFS1750	GCTGTCTGTACATGCCCCAGGAGGACTGGGTTAAACAAAGCTTAACAGCCCCCAGGGCCCCAACCATGGAGTGCGTGACCATGGCGTAAGG	270
1750-Std	
TD6-4G	
CoaV750	
L695121.05A.....	
TNM771K	
MSI-7	
Kern217	
CoaV608	

TBH-28
VR1265
CoaV353

BFS1750 ACTAGAGGTTAGAGGAGACCCCGCTGCAACTTGGCAAGGCCCAACCCGCTCGAAGCTGTAGAGACGGGGGAAGGACTAGAGGTTAGAGG 360
1750-Std
TD6-4G
CoaV750
L695121.05
TNM771K
MSI-7
Kern217
CoaV608
TBH-28
VR1265
CoaV353

BFS1750 AGACCCCTTGCCGTTAACGCAAAACAACAGCATATTGACACCTTGAAAGACAGGAGATC 418
1750-Std
TD6-4G
CoaV750
L695121.05
TNM771K
MSI-7
Kern217
CoaV608
TBH-28
VR1265
CoaV353